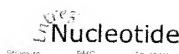


EXHIBIT 1



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GenBank(Full)

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5

Send to

Projection on the feature (#6841)

Show whole Sequence

Features

+

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1: BA000043. Reports *Geobacillus kaustophilus* [gi:56378377]

Links

Features Sequence

LOCUS BA000043 1137 bp DNA linear BCT 04-DEC-2004
 DEFINITION *Geobacillus kaustophilus* HTA426 DNA, complete genome.
 ACCESSION BA000043 REGION: 1613..2749
 VERSION BA000043.1 GI:56378377
 KEYWORDS .
 SOURCE *Geobacillus kaustophilus* HTA426
 ORGANISM *Geobacillus kaustophilus* HTA426
 Bacteria; Firmicutes; Bacillales; Bacillaceae; *Geobacillus*.
 REFERENCE 1
 AUTHORS Takami, H., Takaki, Y., Chee, G. J., Nishi, S., Shimamura, S., Suzuki, H.,
 Matsui, S. and Uchiyama, I.
 TITLE Thermoadaptation trait revealed by the genome sequence of
 thermophilic *Geobacillus kaustophilus*
 JOURNAL (ex) Nucleic Acids Res. 32 (21), 6292-6303 (2004)
 PUBMED 15576355
 REFERENCE 2 (bases 1 to 1137)
 AUTHORS Takami, H., Takaki, Y. and Chee, G.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-2003) Hideto Takami, Japan Marine Science and
 Technology Center, Microbial Genome Analysis Research Group; 2-15
 Natsushima-cho, Yokosuka, Kanagawa 237-0061, Japan
 (E-mail: takami@jamstec.go.jp,
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 Tel: 81-46-867-9643, Fax: 81-46-867-9645)
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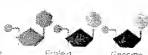
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Features:

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1: NC_006274. Reports *Bacillus cereus* E...[gi:52140164]

Links

Comment Features Sequence

LOCUS NC_006274 1140 bp DNA linear BCT 03-DEC-2005

DEFINITION *Bacillus cereus* E33L, complete genome.

ACCESSION NC_006274 REGION: 1927..3066

VERSION NC_006274.1 GI:52140164

PROJECT GenomeProject:12468

KEYWORDS .

SOURCE *Bacillus cereus* E33L

ORGANISM *Bacillus cereus* E33L
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; *Bacillus cereus* group.

REFERENCE 1 (bases 1 to 1140)

AUTHORS Brettin,T.S., Bruce,D., Challacombe,J.F., Gilna,P., Han,C., Hill,K., Hitchcock,P., Jackson,P., Keim,P., Longmire,J., Lucas,S., Okinaka,R., Richardson,P., Rubin,E. and Tice,H.

TITLE Complete genome sequence of *Bacillus cereus* E33L

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1140)

CONSTRM NCBI Genome Project

TITLE Direct Submission

JOURNAL Submitted (16-SEP-2004) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

REFERENCE 3 (bases 1 to 1140)

AUTHORS Brettin,T.S., Bruce,D., Challacombe,J.F., Gilna,P., Han,C., Hill,K., Hitchcock,P., Jackson,P., Keim,P., Longmire,J., Lucas,S., Okinaka,R., Richardson,P., Rubin,E. and Tice,H.

TITLE Direct Submission

JOURNAL Submitted (14-JUL-2004) Joint Genome Institute, Department of Energy, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from CP000001. COMPLETENESS: full length.

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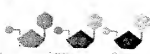
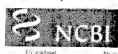
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☐ 1: NC_005957. Reports *Bacillus thuringiensis* [gi:49476684]

Links

Comment Features Sequence

LOCUS NC_005957 1140 bp CNA linear BCT 03-APR-2006

DEFINITION *Bacillus thuringiensis* serovar *konkukian* str. 97-27, complete genome.

ACCESSION NC_005957 REGION: 1928..3067

VERSION NC_005957.1 GI:49476684

PROJECT GenomeProject:10977

KEYWORDS

SOURCE *Bacillus thuringiensis* serovar *konkukian* str. 97-27

ORGANISM *Bacillus thuringiensis* serovar *konkukian* str. 97-27

Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*; *Bacillus cereus* group.

REFERENCE 1 (bases 1 to 1140)

AUTHORS Brettin,T.S., Bruce,D., Challacombe,J.F., Gilna,P., Han,C., Hill,K., Hitchcock,P., Jackson,P., Keim,P., Longmire,J., Lucas,S., Okinaka,R., Richardson,P., Rubin,E. and Tice,H.

TITLE Complete genome sequence of *Bacillus thuringiensis* 97-27

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1140)

CONSTRM NCBI Genome Project

TITLE Direct Submission

JOURNAL Submitted (11-SEP-2004) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

REFERENCE 3 (bases 1 to 1140)

AUTHORS Brettin,T.S., Bruce,D., Challacombe,J.F., Gilna,P., Han,C., Hill,K., Hitchcock,P., Jackson,P., Keim,P., Longmire,J., Lucas,S., Okinaka,R., Richardson,P., Rubin,E. and Tice,H.

TITLE Direct Submission

JOURNAL Submitted (07-JUN-2004) Joint Genome Institute, Department of Energy, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from AE017355. *Bacillus thuringiensis* 97-27 (subsp. *konkukian* (serotype H34)) was originally isolated from a case of severe human tissue necrosis (*Bacillus thuringiensis* subsp. *konkukian* (serotype H34) superinfection: Case report and experimental evidence of pathogenicity in immunosuppressed mice. Hernandez, E, Ramisse, F, Ducourau, J-F, Cruel, T, and Cavallo, J-D. J Clin Microbiol 1998 36(7):2139-2139). *B. thuringiensis* is indigenous to many habitats worldwide; these include soil, insects, deciduous and coniferous leaves (Prediction of insecticidal activity of *Bacillus thuringiensis* strains by polymerase chain reaction product profiles. Carozzi, NB, Kramer, VC, Warren, GW, Ewols, S, and Kosel, MG. Appl Environ Microbiol. 1991 57(11):3057-61). *B. thuringiensis* is an insect pathogen that is widely used as a biopesticide in commercial agriculture. Infection of humans is unusual. The apparent pathogenic properties of *B. thuringiensis* 97-27 are very unusual for *B. thuringiensis*; unlike most *B.*

thuringiensis isolates, this isolate is very closely related to B. anthracis based on phylogenetic analysis (Fluorescent amplified fragment length polymorphism analysis of *Bacillus anthracis*, *Bacillus cereus*, and *Bacillus thuringiensis* isolates. Hill, KK, Ticknor, LO, Okinaka, KT, Asav, M, Blair, M, Bliss, KA, Laker, M, Pardington, PE, Richardson, AP, Tonks, M, Beecher, DJ, Kemp, JE, Kolsto, A-B, Wong, ACL, Keim, P, and Jackson, FJ. Appl Environ Microbiol 70(2):1068-1080. Plasmid and fosmid libraries were prepared at the Joint Genome Institute in Los Alamos (JGI-LANL), NM. Shotgun sequencing was performed at the JGI Production Genomics Facility (JGI-PGF) in Walnut Creek, CA to a coverage of 24x. Finishing was performed at JGI-LANL starting with 83 contigs and 16 scaffolds. Repetitive regions were identified, assembled and finished by manually checking paired reads close to each repeat in the assembly with contigs and then making a subassembly for each repetitive region. Fifty five gaps were closed with primer walks and 16 by PCR. Gene predictions were obtained using Glimmer and tRNAs were identified using tRNAscan-SE. Basic analysis of the gene predictions was performed by comparing coding sequences against the Pfam, BLOCKS and Prodom databases. Gene definitions and functional classes were added manually by a team of annotators at JGI-LANL, using BLAST results in addition to information from the basic analysis. A total of 5540 features have been annotated on the sequence record.

COMPLETENESS: full length.

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Features: ☒ CDD

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☐ 1: EAR74115. Reports DNA polymerase III...[gi:89154071]BLink, Conserved
Domains, Links

Comment Features Sequence

LOCUS EAR74115 381 aa linear BCT 03-MAR-2006

DEFINITION DNA polymerase III, beta chain [Bacillus weihenstephanensis KBAB4].

ACCESSION EAR74115

VERSION EAR74115.1 GI:89154071

DESCRIBE accession AAQY01000054.1

KEYWORDS

SOURCE Bacillus weihenstephanensis KBAB4

ORGANISM Bacillus weihenstephanensis KBAB4
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1 (residues 1 to 381)

AUTHORS Lapidus, A., Goltzman, E., Copeland, A., Lucas, S., Barry, K., Deter, J.C., Glavina del Rio, T., Hammon, N., Israni, S., Dalin, E., Tice, H., Bruce, D., Pitluck, S., Richardson, P., Auger, S., Galleron, N., Sanchis, V., Gohar, M., Brousseau, V., Brillard, J., Guinebretiere, M.-H., Ehrlich, S.D., Lereclus, D., Aymerich, S., Nguyen-the, C. and Sorokin, A.

CONSRM US DOE Joint Genome Institute (JGI-PGF)

TITLE Sequencing of the draft genome and assembly of Bacillus weihenstephanensis KBAB4

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 381)

AUTHORS Larimer, F. and Land, M.

CONSRM US DOE Joint Genome Institute (JGI-ORNL)

TITLE Annotation of the draft genome assembly of Bacillus weihenstephanensis KBAB4

JOURNAL Unpublished

REFERENCE 3 (residues 1 to 381)

AUTHORS Lapidus, A., Goltzman, E., Copeland, A., Lucas, S., Barry, K., Deter, J.C., Glavina del Rio, T., Hammon, N., Israni, S., Dalin, E., Tice, H., Bruce, D., Pitluck, S., Richardson, P., Auger, S., Galleron, N., Sanchis, V., Gohar, M., Brousseau, V., Brillard, J., Guinebretiere, M.-H., Ehrlich, S.D., Lereclus, D., Aymerich, S., Nguyen-the, C. and Sorokin, A.

CONSRM US DOE Joint Genome Institute (JGI-PGF)

TITLE Direct Submission

JOURNAL Submitted (02-MAR-2006) US DOE Joint Genome Institute, 2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA

COMMENT UFL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson (microbes@cuba.jgi-psf.org)
Draft sequencing done at US DOE Joint Genome Institute
Source DNA and bacteria available from Alexei Sorokin (alexei.sorokin@jouy.inra.fr)
The JGI and collaborators endorse the principles for the distribution and use of large scale sequencing data adopted by the larger genome sequencing community and urge users of this data to

follow them. It is our intention to publish the work of this project in a timely fashion and we welcome collaborative interaction on the project and analysis.

(<http://www.ncbi.nlm.nih.gov/page.cgi?pageID=10506376>)

Notes:

Bacillus weihenstephanensis KBAB4 was originally isolated from forest soil near Versailles, France, and was originally identified as *Bacillus cereus* (Villas-Boas et al, Appl Env Microbiol, 2002, 68, 1414). More detailed phylogenetic analysis, using MLST, of the Versailles Collection of *B. cereus* and *B. thuringiensis* strains revealed that the strain grows at low temperature (60C) and clusters with many other strains able to grow at low temperatures, including the independently isolated and characterized strains WSB010204 and WSB010206 (Sorokin et al, Appl Env Microbiol, 2006, 72, 1569). The latter two strains are the type strains of a newly recognized species in the *B. cereus* group able to grow in cold and having the species name *Bacillus weihenstephanensis* (Lechner et al, Int. J. Syst. Bacteriol, 1998, 48, 1373). Since, by MLST, KBAB4 is very closely related to WSB010204 and represents many other psychrotrophic strains, it was assigned a species name *Bacillus weihenstephanensis* and the strain KBAB4 should also be considered as a type representative of this species.

Method: conceptual translation.

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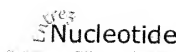
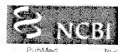
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1: NC_000964. Reports *Bacillus subtilis*...[gi:50812173]

Links

Comment Features Sequence

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 VERSION NC_000964.2 GI:50812173
 PROJECT GenomeProject:76
 KEYWORDS complete genome.
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 ORGANISM *Bacillus subtilis* subsp. *subtilis* str. 169
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 REFERENCE 1 (bases 1 to 1137)
 AUTHORS Kunst, F., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G.,
 Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S.,
 Borries, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C.,
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 Yoshida, K., Yoshikawa, H.F., Zumbstein, E., Yoshikawa, H. and
 Danchin, A.
 TITLE The complete genome sequence of the gram-positive bacterium
Bacillus subtilis
 JOURNAL Nature 390 (6657), 249-256 (1997)
 PUBMED 9284377
 REFERENCE 2 (bases 1 to 1137)
 CONSPMT NCBI Genome Project
 TITLE Direct Submission

JOURNAL Submitted (12-OCT-2001) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

REFERENCE 3 (bases 1 to 1137)

AUTHORS Munst, F., Ogasawara, N., Yoshikawa, H. and Ganchin, A.

TITLE Direct Submission

JOURNAL Submitted (18-NOV-1997) Institut Pasteur, Regulation de l'Expression Genetique, 28 rue du Docteur Roux, Paris Cedex 15 75124, France

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from AL009126. On Jul 29, 2004 this sequence version replaced gi:16077070.

FEATURES

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CDS 1..1137

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ORIGIN

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Comment Features Sequence

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 ACCESSION YP_089686
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 DBSCURCE REFSEQ: accession NC_006322.1
 KEYWORDS .
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 ORGANISM Bacillus licheniformis ATCC 14580
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 REFERENCE 1 (residues 1 to 378)
 AUTHORS Veith,B., Herzberg,C., Steckel,S., Feesche,J., Maurer,K.H., Ehrenreich,P., Baumer,S., Henne,A., Liesegang,H., Merkl,R., Ehrenreich,A. and Gottschalk,G.
 TITLE The complete genome sequence of Bacillus licheniformis DSM13, an organism with great industrial potential
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 378)
 CONSRM NCBI Genome Project
 TITLE Direct Submission
 JOURNAL Submitted (28-SEP-2004) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA
 REFERENCE 3 (residues 1 to 378)
 AUTHORS Veith,B., Herzberg,C., Steckel,S., Feesche,J., Maurer,K.H., Ehrenreich,P., Baumer,S., Henne,A., Liesegang,H., Merkl,R., Ehrenreich,A. and Gottschalk,G.
 TITLE Direct Submission
 JOURNAL Submitted (30-APR-2004) Institute of Microbiology and Genetics, Georg August University Goettingen, Goettingen Genomics Laboratory, Grisebachstr. 8, Goettingen D-37077, Germany
 COMMENT VALIDATED REFSEQ: This record has undergone preliminary review of the sequence, but has not yet been subject to final review. The reference sequence was derived from RAU898993.
 Method: conceptual translation.
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EXHIBIT 2

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# Rundate: Mon Jul 31 07:00:44 2006
# Align_format: srspair
# Report_file: /ebi/extern/old-work/needle-20060731-07004323238664.output
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# 2: G_kaustophilus
# Matrix: EBL0SUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
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# Length: 1138
# Identity: 987/1138 (86.7%)
# Similarity: 987/1138 (86.7%)
# Gaps: 147/1138 (12.9%)
# Score: 5832.0
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#####
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10266505_1

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SEQ173	460	gtcgtcatccctggaaaaagtcctaatgagctcagcaaaattttggatga	509
G_kaustophil	601	gtcgtcatccctggaaaaagtcctaatgagctcagcaaaattttggatga	650
SEQ173	510	cggcaaccacccgggtggacatcgtcatgacagccaatcaagtgcattta	559
G_kaustophil	651	cggcaaccacccgggtggacatcgtcatgacagccaatcaagtgcattta	700
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G_kaustophil	701	aggcagagcaaccttctctcttttcccggtgctgtgacggcaactatccg	750
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G_kaustophil	751	gagacggcccgcttgattccacagaaagcaaacgaccatgatcgtcaa	800
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G_kaustophil	801	tgcataaagagttttctgcaggcaatcgaccgagcgtcttcttctctcgag	850
SEQ173	710	aaggaaaggaaacaacgttgtgaaactgaagacgcttctctggaggaatgctc	759
G_kaustophil	851	aaggaaaggaaacaacgttgtgaaactgaagacgcttctctggaggaatgctc	900
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G_kaustophil	901	gaaattttctcgatttctccggagatcgggnaagtgacggagcagctgcga	950
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G_kaustophil	951	aacggagctctcttgaaaggggaagagttgaacatttcgttcagcgcgaat	1000
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G_kaustophil	1050	cttcaactggggccatgcggcgcttctgttgcgcccgcttcaataccgatt	1099
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##

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 # 2: B_cereus
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 # Similarity: 654/1146 (57.1%)
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 # Score: 3294.5
 #

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B_cereus	251	aaattgtaaaaaaataactaaagaactgtgaaatttctgtggaat	300
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B_cereus	301	catttgatgacaaaaataacttctggaatcagagtttaatttaaatgg	350
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B_cereus	650	atgagctctgaag - aaatggttagatctcgttatctagcagatcaagat	697
SEQ173	554	tatttaagcgcgagacacctctctctctctcccgagctcgttcagcgcaac	603
B_cereus	698	tatttcgtacaaaacatttattattctctctcaagattgttagaaggaaat	747
SEQ173	604	tatccggagacggccgcgttatttcacacagaagaacaaaagaccatgat	653
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B_cereus	897	aatgctagaaattttctcnaattcaccagaaatcgggaagtagtagaag	946
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# Aligned_sequences: 2
# 1: SEQ173
# 2: B_thuringiensis
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# Gap_penalty: 10.0
# Extend_penalty: 0.5
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# Length: 1148
# Identity: 655/1148 (57.1%)
# Similarity: 655/1148 (57.1%)
# Gaps: 164/1148 (14.3%)
# Score: 3260.0
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B_thuringiens	151	atttcgattgaatcttttatcccgatgaagaggatggaanaaattgt		200
SEQ173	60	tgatgtgaaaagaccggggagcatcgctactgcaggcgcgctttttctctg		109
B_thuringiens	201	agaagtataaacatcaggaaagtattgtttacaggttaaatatttagtg		250
SEQ173	110	aaatcgtgaaaaaactgcgcgaacaaacggtggaaa--tcgaaacggaag		157
B_thuringiens	251	aaattgtataaaaaattgcgcgaagaacgtgagaatttc-tgctgaaaa		299
SEQ173	158	acaaactttttgacgatcatcogctcggggcactcagaattccgcctcaat		207
B_thuringiens	300	tcatt-ttaatgacaaaaataactcttgggaaatcagaatttaatttaaat		348
SEQ173	208	gggctaaacgcccagcaaatatccgcgcctgcgcgaattggaagaagaaa		257
B_thuringiens	349	ggtttagattctgcagaatatccattgttaccacaaattgagaacatca		398
SEQ173	258	cgtgtttcaaatcccgctgattttatgaaaacgctgattcgcgaacgg		307
B_thuringiens	399	tgtttttaagattccacagatttactttaacatatgatnagacaaactg		447
SEQ173	308	tgttcgcgctttctacatcggaacgcgcgcgaactcttgacaggtgtcaac		357
B_thuringiens	449	tatttgcagctctccactctgaaacaaagacaaatcttgacaggtgtcaac		498
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B_thuringiens	499	tggaaaggtatataacagcgaactaacttgattgtctacagatagtcacag		548

SEQ173	408	cttagccctgcccgaagtgaaaattga--gtc-ggaaaaatgaagatcat	454
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SEQ173	455	acaac-gtcgtcatccctggaaaaagttcttaaatgagctcagcaaaatttt	503
B_thuringiens	598	gcaaatgttgttatttcggggaaaagcttaaatgaattgaagcaaaattct	647
SEQ173	504	ggatga--cgccacccaccggctggacatcgtcatgacagccaatcaagt	551
B_thuringiens	648	agatgagctctgnag--aaatggtagatctgttattacggagtagtaagt	695
SEQ173	552	gctattttaaggccgagcacctctctctctctctctctctccgctgttgaggga	601
B_thuringiens	696	attatccgtacaaaacatttatattctctcaagattgttagaggaa	745
SEQ173	602	actatccggagacggcccgcttgattccaacagaagaacaaacgaccatg	651
B_thuringiens	746	attatccgtacaaaacatttatattctctcaagattgttagaggaa	795
SEQ173	652	atcgtcaatgcmaaaagagtttctgcaggcaatcgaccgagcgtctctgtct	701
B_thuringiens	796	tttgtaaatacaaaagaatttttacaagcaattgactcgtcatctctgtt	845
SEQ173	702	tgcctcgagaaggaaagaaacagcttgtgaaactgacgacgcttccggag	751
B_thuringiens	846	agctagagatggctgtaataatgttgtgaaattatcaac-tttagagcag	894
SEQ173	752	g-aatgctcgaaatttcttcgatttctcc-gagatcgggaaggt-gacgg	798
B_thuringiens	895	gcaatgctagaaatttcttcgaattccacagaatcggaaaagttagtaga	944
SEQ173	799	agcagctgcacacggaggtctcttgaaggggaagagttgaacatttcgttc	848
B_thuringiens	945	agaagtt-caatgtgaaaaagtagatggagaagagttaaaaatatcttt	993
SEQ173	849	agcgcgaatatatgatggacgcgttgcggcgcttgatggaacagacat	898
B_thuringiens	994	agtcgcaaaatatatgatggagcactaaaggcatttagatagtactga-aa	1042
SEQ173	899	ttcaaatcagcttctactggggccatcgggccgttctctgttgcgccgctt	948
B_thuringiens	1043	ttgaagattagctttactggagcaatgagaccattcttaattctgacgga	1092
SEQ173	949	ca-accgattcgatgcttcttcagctcattttgcgggtgagaacatat	992
B_thuringiens	1093	aatgatgaatccattattcaattattttaccggttcgtactactacaa	1140

SEQ173	360 gaaagttgaacatggcgagcttctgtgacacgagcagcagctcatcgct	409
B_weihensteph	501 gaaggtatataacacgagcctaacttgtattgcaacagatagtcacagac	550
SEQ173	410 tagccatggcgaaagtgaattga---gtcggaatgaag-----tat	451
B_weihensteph	551 tagcacttcgttaagcaaaaatcgaggggtataatatgacgatgaattt	600
SEQ173	452 catac-aacgcgctcatccctggaaaaagttctaatgagctcagcaaaaat	500
B_weihensteph	601 caagcgaatgtcgcttattctcggtgaagagcttaagtgaatttaagtaaat	650
SEQ173	501 tttagatga--cggaacacaccccggtggacatcgctcatgacagccaatca	548
B_weihensteph	651 tctagatgaatctgaag--aaatggtagatcgcttattacggaggtatca	698
SEQ173	549 agtgcatttttaagggcgagcaccttctctcttttcccggtgctgtgaag	598
B_weihensteph	699 agtatatttcgtacaaaacattttattattcttctcaagattattagaag	748
SEQ173	599 gcaactatccggagacggcccgcttgattccaacagaaagcaaaaacgac	648
B_weihensteph	749 gaatttatccagatcacacgcgtttaattccagctgaagtaaaactgat	798
SEQ173	649 atgatcgctcaatgcaaaagagtttctgcaaggcaatcgacagcgctcctt	698
B_weihensteph	799 atatttgttaaatcaaaaagaatttttacaagcgattgatcgctgctgctt	848
SEQ173	699 gottgctcgagagaaggaaggaacaaogttgtgaaactgacgacgcttcttg	748
B_weihensteph	849 gttagcaagagatggctcgtaacaacggttggttaaatatcgacattagaac	898
SEQ173	749 gaggaatgctogaaaatttcttgcgatttctcc-gagatcgggaaagtgaag	797
B_weihensteph	899 aacagatggttagagatttcttogaatgcaccagaatcggaagtagta	948
SEQ173	798 gagcagctgcacaaogagctctcttgaaggggaagagttgaacatttcgtt	847
B_weihensteph	949 gaagaggttcaatgtgaaaatgtagatggagaagaattaaaaatatcttt	998
SEQ173	848 cagcgogaaaatatatgatggacgcttgcggcgcttgatggaacagaca	897
B_weihensteph	999 tagtgcaaaaatatatgatggacgcatgaaggcttttagacagtcacaga-a	1047
SEQ173	898 ttccaatcagcttcaactggggccatcgggcgcttctgtgcgcccgcgt	947
B_weihensteph	1048 attaaagtttagttttactggagcgatgagacgcttttcaattgcacagct	1097
SEQ173	948 tca-accgattcgatgcttcaagctcatattttgcgggtgagaacatat	992
B_weihensteph	1098 aaatgatgattccattatccaatttaattttaccagtcgtaactactaa	1146

```

# Needle alignment program
# Program: needle
# Rdate: Mon Jul 31 07:06:37 2006
# Align_format: srspair
# Report_file: /ehi/extern/old-work/needle-20060731-07063643205179.output
#

```

```

#
# Aligned_sequences: 2
# 1: SEQ173
# 2: B_subtilis
# Matrix: BLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1145
# Identity: 682/1145 (59.6%)
# Similarity: 682/1145 (59.6%)
# Gaps: 161/1145 (14.1%)
# Score: 3577.5
#

```

```

SEQ173      1                                aatccgac      9
B_subtilis 101 aaattgttgcatcagatgatggagatcctttacagggagtgcactcagat 150
SEQ173      10 atttcaattgaatcggtttatccgcttgaaaaagaaggcaagtgtcgct 59
B_subtilis 151 atttctattgaatccttcatccaaaagaagaaggagataaagaatcgt 200
SEQ173      60 tgatg-tgaaaagaccggggagcactcgactgcaggcgctgtttctct 108
B_subtilis 201 cactattgaacagccc-ggaagcatcgtttacaggctcgctttttagt 249
SEQ173      109 gaaatcgtgaaaaaactgccgcaacaacggtggaatcgaa-acggaag 157
B_subtilis 250 gaaattgtaaaaaattgccgatggcaactgtagaattgaagtcacaaa 299
SEQ173      158 acaactctttgacgatcatcgctcggggcactcagaattccgcctcaat 207
B_subtilis 300 tcag-tatttgacgattatccggtctggtaaaagctgaatttaattcaaac 348
SEQ173      208 gggctaaacgccgacgaatatccgcgcttgcgcgaattgaagaagaaaa 257
B_subtilis 349 ggactggatgctgatgaatatccgcacttgcgcgagattgaagagatca 398
SEQ173      256 cgtgtttcaaatcccgctgatttattgaaacccgagttgcgcaacgg 307
B_subtilis 399 tgcgattcagatcccaactgatttgttaaaaatcttaatcagacaaacag 448
SEQ173      308 tgttgcgcgtttctacatcggaacgcgcgcacatcttgacaggtgtcaac 357
B_subtilis 449 tatttgcagtgctccacotcagaacacgcgcctatcttgacaggtgttaac 498
SEQ173      358 tggaaagtgaacatggcgagctgtgtctgcacagcgacgacagtcatcg 407
B_subtilis 499 tggaaagtggagcaaaagtgaattattatgcactgcaacggatgacccacg 548

```

SEQ173	408	cttagccatgcgcgaagtgaattgagtcggaatgaagatcataca	457
B_subtilis	549	tctgtcattaaagggcgaactgatattcagaagacagacttata	598
SEQ173	458	acgtcgatccctggaaaaagtcttaattgagctcagcaaaattttggat	507
B_subtilis	559	acgtcgatgattccggaaaaagttaactgaactcagcaagattttagat	648
SEQ173	508	gacggcaaccacccgggtggacatcgatcacagccaatcaagtgtatt	557
B_subtilis	649	gacacccaggaacttctgatattcgatcacagaaacccaagttctgtt	698
SEQ173	558	taaggccgagacactttctc-ttctttcccgctggttgacggcactat	606
B_subtilis	699	taag-cgaaaaacgtctgttctcctcagcgcttctggacgggaattat	747
SEQ173	607	cgggagacggcccgcttgattccaaacagaagcaaacgacatgatcgt	656
B_subtilis	748	ccagacacaaccagcctgattccgcaagacagcaaacagaaatcattgt	797
SEQ173	657	caatgcgaagagtttctgcaggcaatcgacagcgctccttgcctgtc	706
B_subtilis	798	gaacacaaaagatttctctcaggccattgatcgtgcactctctttagcta	847
SEQ173	707	gagaagggaaggaaacacgttgtgaactgacgacgcttcttgagggaatg	756
B_subtilis	848	gagaggggacgcaacaacgttgtgaactgtccgcaaacac-ggctgaatc	896
SEQ173	757	c-tcgaaatttctcgatttctcc-gagatcgggaaa-gtgcggagcag	803
B_subtilis	897	cattgaaatttctccaattcgccagaatcggtaaagttgtggaagcaa	946
SEQ173	804	ctgcaaacggagctctcttgaagggaagagttgaacatttctgtcagcgc	853
B_subtilis	947	tgt-ttgcggatcaaatgaaggtgagggaattaaatatctcttttagtcc	995
SEQ173	854	gaaatatatgatggacgctgtcgggcgctgtgatggaacagacatttcaa	903
B_subtilis	996	aaaatatatgctggatgcactaaaggtgcttgaaggagcaga-aatcgc	1044
SEQ173	904	atcagcttcaatggggccatcgccgcttctgttgcgcgcgcttcaacc	953
B_subtilis	1045	gtaagctttacaggcgcgaatgagacacttcttaattcgcaacg--cgaat	1092
SEQ173	954	gat---tcgatgcttcagctcatttgcgggtgagaacatat	992
B_subtilis	1093	gatgaaacgattgtacagcttatcttctgtcagaactatttaa	1137

```

# Program: needle
# Runcdate: Mon Jul 31 07:09:46 2006
# Align_format: ssepair
# Report_file: /ebi/externserv/old-work/needle-20060731-07094578887427.Output
#

```

```

#
# Aligned_sequences: 2
# 1: SEQ173
# 2: B_licheniformis
# Matrix: SELOSSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1161
# Identity: 704/1161 (60.6%)
# Similarity: 704/1161 (60.6%)
# Gaps: 193/1161 (16.6%)
# Score: 3657.5
#

```

```

SEQ173      1                                aattccgac      9
               .|||||
B_licheniform 101 aaatcggtggcctctgatgaaggggtctctctgacagggcagcgattccgat 150
               .|||||
SEQ173      10 atttcaattgaatcggtttattccgcttgaaaagaagggcaagtt---gct 56
               |||||
B_licheniform 151 atttcgattgaatcggtttatccg---aaagaagacggcgatttagagat 197
               .|||||
SEQ173      57 cgttg-atgtgaaaagaccggggagcatcgtactgcaggcgcgctttttc 105
               |||..
B_licheniform 198 cgtgacaattgaacagccc-ggcagcattgtgcttcaagccggtttttc 246
               .|||||
SEQ173      106 tctgaaatcgtgaaaaaactgcgcgaacaaacggtggaaatcgaaacgga 155
               .|||||
B_licheniform 247 agtgaatgtgcaaaaagctgcgcgatgtcaacagtggaatcgaggttca 296
               .|||||
SEQ173      156 agacaaacttttgacgatcatccgctcggggactcagaattccgctca 205
               |..|
B_licheniform 297 aaatcaatacttaacgatcatccgctcgggcaagcagagtttaacttaa 346
               .|||||
SEQ173      206 atgggctaaacgcgcgaagaatattccgcgctgcgcgaattgaagaagaa 255
               |..|
B_licheniform 347 acggtttggatgcaagcgaatattccgcttttgcgcgaattgaagagatc 396
               .|||||
SEQ173      256 aacgtgtttcaaatcccgctgatttattgaaaacggtgattcgccaaac 305
               .|||||
B_licheniform 397 cagcgttttcaaatccgacgcatctgctgaaaaacactgatccgcaaac 446
               .|||||
SEQ173      306 ggtgttcgcggtttctacatcggaaaacgcgcgaatcttgacaggtgtca 355
               .|||||
B_licheniform 447 cgtttttgcagtgcccaactcagaacacgcgcgaatcttgacaggtgtca 496
               .|||||
SEQ173      356 actggaagttgaacatggc---gaagctgtctgtgcacagcagcagcagc 402
               |||||
B_licheniform 497 actggaatgt---cac-tggcggtgaattaatatgcactgcaacggatagt 543
               .|||||

```

SEQ173	403	catcgcttagccatgcgcaaaagtgaattgag-tcggaa--aatgaagt	449
B_licheniform	544	catc-----gtcttgcgtaag-gaaagctaagctgcacattaacgaaga	587
SEQ173	450	--atcatacaacgtcgctcatccctggaaaagctcttaatgagctcagca	496
B_licheniform	588	cagttcatacaatgtcgctcatcccgaaaagcttaacgagctcagca	637
SEQ173	497	aaattttggatgagcgcaacc--accgggtggacatcgctcatgacagca	544
B_licheniform	638	aaatccttgatgac--catcaggagcttgatattgtgattacgaaa	685
SEQ173	545	atcaagtgcttatttaaggcgagcacctctctctctctcccgctgctt	594
B_licheniform	686	cacaagtgctgtttaaacaacaaacgttctgtttttctccagcttctt	735
SEQ173	595	gacggcaactatccggagagcgcccgcttgattccaaacagaagcaaac	644
B_licheniform	736	gacggaaactatccggatacgaacccgctgattctcaggaaagcaaac	785
SEQ173	645	gacctgatcgtaaatgcaaaagagtttctgagggcaatcgacagagct	694
B_licheniform	786	gaacttgatgtcaactactaaggaaatttctccagcgatcgacagggctt	835
SEQ173	695	ctttgctt--gctcgagagaaggaaacacgttgtgaaactgacgag	741
B_licheniform	836	c---gcttttggcgagagaaggacgaacacgttgtgaaacttctc--cg	880
SEQ173	742	cttc--ctggaggagatgctcgaaatttcttcgattctcc-gagatcggt	788
B_licheniform	881	cagcgcccaatgagtcgatcgaaatttctcacaactctccggaatcgga	930
SEQ173	789	aaag-tgacggagcagctgcaaacggagctctcttgaaggggaagagttga	837
B_licheniform	931	aaggttggtgaaacgg-tgaatgccgagcagatcgaaagggaagacttaa	979
SEQ173	838	acatttctgttcagcgcaaatatgatggacgcgcttcggtggcgcttgat	887
B_licheniform	980	agatatccttttagtcgcaaatatgatggtgacccctaaagtcttgaa	1029
SEQ173	888	ggaacagacatttcaaatcagcttcaactggggccatgcgcgcgttctgt	937
B_licheniform	1030	ggagaggaca-ttcattgtaagcttcacagcgctatgagcgctttctga	1078
SEQ173	938	tgcgcccgcgttcaaa---ccgattcgatgcttcagctcaattttgcggta	984
B_licheniform	1079	tcgtaacgc--cgaatgacgattcgatgctcaatttaattctctgtcc	1126
SEQ173	985	gaacatat	992
B_licheniform	1127	ggacttataa	1137

EXHIBIT 3

CLUSTAL W (1.83): Multiple Sequence Alignments

Sequence format is Pearson
 Sequence 1: SEQ174 334 aa
 Sequence 2: G_kaustophilus 378 aa
 Start of Pairwise alignments
 Aligning...
 Sequences (1:2) Aligned. Score: 97
 Guide tree file created: [//ebi/extern/cluster-work/interactive/clusterw-20060731-05543637.dnd]
 Start of Multiple Alignment
 There are 1 groups
 Aligning...
 Group 1: Sequences: 2 Score:6996
 Alignment Score 1906
 CLUSTAL-Alignment file created [//ebi/extern/clusterw-work/interactive/clusterw-20060731-05543637.aln]

```

SEQ174 -----NSDIIIESIFIPL 13
G_kaustophilus MNISIDREALAKSVQDVMAVSTRRTTIFILTGIKLTATASGVILTGSSEIS-IESIFIPL 69
                      :*** *****

SEQ174 EKEGKLLVDVKRPGSIVLQARFFSEIVKKLPQQTVEIETEDNFLTIRSGHSEFRNLGNL 73
G_kaustophilus EKEGKLLVDVKRPGSIVLQARFFSEIVKKLPQQTVEIETEDNFLTIRSGHSEFRNLGNL 119
*****

SEQ174 ADEYFRLPQIEEENVFQIPADLLKTVIRQTVFAVSTSETRPILTGUNVKVHSELVCTAT 133
G_kaustophilus ADEYFRLPQIEEENVFQIPADLLKTVIRQTVFAVSTSETRPILTGUNVKVHSELVCTAT 179
*****

SEQ174 DSHRLAMRAVKKIESENEVSYNVVIPIGKSLNELSKIIILDDGNHPEVDIVMTANQVLFKAEN 193
G_kaustophilus DSHRLAMRAVKK-IESENEVSYNVVIPIGKSLNELSK-ILDDGNHPEVDIVMTANQVLFKAEN 237
*****

SEQ174 LLFFSRLLDGNYPETARLIPTESKITMIIVNAKEFLQAI DRASLLAREGNRVVKKLTILPG 253
G_kaustophilus LLFFSRLLDGNYPETARLIPTESKITMIIVNTKEFLQAI DRASLLAREGNRVVKKLTILPG 297
*****

SEQ174 GMLEISSISPEIGKVTEQLQTESLEGEELNISFSAKYMMDALRALDGTDIQISFTGAMRP 313
G_kaustophilus GMLEISSISPEIGKVTEQLQTESLEGEELNISFSAKYMMDALRALDGTDIQISFTGAMRP 357
*****

SEQ174 FLLRPLHTOSMLQLILPVRTY 334
G_kaustophilus FLLRPLHTOSMLQLILPVRTY 378
*****

```


CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
 Sequence 1: SEQ174 334 aa
 Sequence 2: B_thuringiensis 379 aa
 Start of Pairwise alignments
 Aligning...
 Sequences (1:2) Aligned. Score: 70
 Guide tree file created: [/ebi/extern/cluster-work/interactive/clusterw-20060731-06031038.dnd]
 Start of Multiple Alignment
 There are 1 groups
 Aligning...
 Group 1: Sequences: 2 Score:6155
 Alignment Score 1367
 CLUSTAL-Alignment file created [/ebi/extern/clusterw-work/interactive/clusterw-20060731-06031038.aln]

```

SEQ174 -----NSCISI-IIESFIPLE 14
B_thuringiensis MRFSIQMDYLVRSVQDVMKAVSSRTTIPILTGIKVVAEEGVTLTGSCADISIESFIPVE 60
                  ** * *****:

SEQ174 KEGKLLVDVKRFSGIVLQARFSEIVKKLPQQTVEIETEDNFLTIRSGHSEFRLNGLNA 74
B_thuringiensis EDGKEIVEVKQSGSIVLQARYFSEIVKKLPKETVELSVENHLMITKISGKSEFNGLDS 120
                  :*: **::*****:*****:*****:*** * **::*****:

SEQ174 DEYFRLPQIEENVPQIPADLLKTVIRQTVPFVSTSETRPILTGVMWVKVEHGLVCTATD 134
B_thuringiensis AEYFLLPQIEENHVFRIPTDLLKHMIRQTVPFVSTSETRPILTGVMWVKVYNSELTCIATD 160
                  *** *****:***:***:*****:*****:*****:***:***

SEQ174 SHRLAMRAVKIIESENEVSYNVVPKSKLNELSKIILDDGNHPVDIVMTANQVLFKAHL 194
B_thuringiensis SHRLALRAKAKIEGIVDEFQANVVPKSKLNELSK-ILDESEEMVDIVITEYQVLFRTKHL 239
                  *****:***:***:*****:*****:***:*** *****:

SEQ174 LFFSRLLDGNYPETARLIFTESKTTMIVNAKEFLQAI DRASLLAREGRNNVVKLTLPGG 254
B_thuringiensis LFFSRLLDGNYPDTTRLIPAESKTDIFVNTKEFLQAI DRASLLARDGRNNVVKLTLEQA 299
                  *****:***:***:***:*****:*****:*****:***

SEQ174 MLEISSISPEIGKVTEQLQTESLEGEELNISFSKAKYMMDALRALDGDIDQISFTGAMRPF 314
B_thuringiensis MLEISSNSPEIGKVVEEVOCEKVDGEELKISFSKAKYMMDALKALDSTEIKISFTGAMRPF 359
                  *****:***:***:*****:*****:***:*** *****:

SEQ174 LRLFLHTDSMLQLILPVRTY 334
B_thuringiensis LRTVNDESIQLILPVRTY 379
                  *:***:***:*****
    
```

Sequence format is Pearson

Sequence 2: 2_weihenstephanensis 361 aa

Aligning...

```
Guide tree      file created:  /ebi/extern/clusterw-work/interactive/clusterw-
#####
```

Start of Multiple Alignment

Aligning...

Alignment Score 1374

CLUSTAL-Alignment file created [/ebi/extern/clusterw-work/interactive/clusterw-20060731-06054661.pain]

11766-525

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
 Sequence 1: SEQ174 334 aa
 Sequence 2: B_subtilis 378 aa
 Start of Pairwise alignments
 Aligning...
 Sequences (1:2) Aligned. Score: 69
 Guide tree file created: [/ebi/extern/cluster-work/interactive/clusterw-20060731-06092781.dnd]
 Start of Multiple Alignment
 There are 2 groups
 Aligning...
 Group 1: Sequences: 2 Score: 6121
 Alignment Score 1379
 CLUSTAL-Alignment file created [/ebi/extern/clusterw-work/interactive/clusterw-20060731-06092781.aln]

```

SEQ174      -----NSDISIIIESFIPL 13
B_subtilis  MKFTIQKDLRVESVQDVLKAVSSRTTTPILTGIKIVASDDGVSTGSDSDIS-IESFIPIK 59
              :****
SEQ174      EKEGKLLVDVKKRPGSIVLQARFFSEIVKKLPQOTVEIETEDNFLTIIIRSGHSEFLNGLN 73
B_subtilis  EEGDKIEVITIEQPGSIVLQARFFSEIVKKLPMTATVEIVQNOYLTIIIRSGKAEFNLGLD 119
              *:.* :*****
SEQ174      ADEYPRLPQIEENVPQIPADLLKTVIRQTVFAVSTSETRPILTGVNWKVEGELVCTAT 133
B_subtilis  ADEYPHLPQIEEHAIQIPTDLLNLIRQTVFAVSTSETRPILTGVNWKVEQSEILCTAT 179
              *****:.*:****
SEQ174      DSHRLAMRKVKIIESENEVSYNVVIPIGKSLNELSKIILDDGNHPVDIVMTANQVLFKAEN 193
B_subtilis  DSHRLALRAKALDIFE-DRSYNVVIPIGKSLTELSK-IILDDNQELVDIVITETOVLFKARN 237
              *****:.* :*****
SEQ174      LLFFSRILLDGNYPETARLIPTESKTTMIVNAKEFLQAIADRASLLAREGRNNVVKLTPLPG 253
B_subtilis  VIFFSRILLDGNYPOTTSLIPQDSKTEIIVNTKEFLQAIADRASLLAREGRNNVVKLSAKPA 297
              *****:.* :*****
SEQ174      GMLIEISSISPEIGKVTEQLQTESLEGEELNISFSKAYMDALRALDGTDIQISFTGAMRF 313
B_subtilis  ESTIEISSISPEIGKVVEAIVADQIEGEELNISFSKAYMLDALKVLEGAEIRVSFTGAMRF 357
              *****:.* :*****
SEQ174      FLRLPLHTDSMLQLILPVRTY 334
B_subtilis  FLIRTPNDEITVQLILPVRTY 378
              **:.* :*****
    
```

Sequence format is Pearson

334 83

378 4a

Aligning...

Guide tree

Start of Multiple Alignment

Aligning...

Alignment Score 1371

SEQ174

-----NSDISIIESFIPL 13
MKFTIQKDLVESVQDVLKAVSSRTTIPILTGIVASDEGVSLTGSDDIS-IESFIPK 59

SEQ174

```

EKEGKLLVDVKRPGSIVLQARFFSEIVKKLPQOTVEIETEDNFLTIIIRSGHSEFRNLNCLN 73
EDGDLEIVTTIEQPGSIVLQARFFSEIVKKLPMSSTVEIVQNOYLTIIIRSGKAEFNLNGLD 119
* . . : * ::*****.*****.*****.*****.*****.*****.*****.

```

SEO174

```

ADEYPRLPQIEEENVQFIPADLLKTVIRQTFVAVSTSETRPILTGWNWKEHGLVCTAT 133
ASEYPLLQIEEHHAQIFETDLLKNLRQTFFAVSTSETRPILTGWNWNTGGELICTAT 179
*. ** * *. . : . ** : * . : * * * * * * * * * * * * * * * * * * * * *

```

SEQ174

DSHRLAMRKVKIIESENEVSNVNVIPGKSLNELSKIILDDGNHPVDIVMTANQVLFKAER 193
DSHRLALRKAKLDINE-DSSNVNVIPGKSLTELSK-ILDDHQELVGVITETQVLFKTKN 237
*****:

SEQ174

LLFFSRLLDGNYPETARLIPTESKTTMIVNAKEFLQAIDRASLLAREGRNNVVKLTTLPG 253
VLFFSRLLDGNYPDNRILPOEKTNLIVNPKFELQAIDRASLLAREGRNNVVKLSAAAN 297

:*****:* * * *

SEO174

```

GMLEISSISPEIGKVTEQLQLTESLEGEELNISFSKAYMMDALRALDGTDIQISFTGAMRP   313
ESIEISSNSPEIGKV/VETVNAEQLEGEDLKI$FSPKYMLDALKVLEGEDIHVSFTGAMRP   357
***** *::*:*****:*****:*****:*****:*****

```

EQ174

```
FLLRFLHTDSMLQLILPVRTY 334  
FLIRTPNDDSIQILIPVRTY 378  
*: *: : *::*****
```